

REMARKS

Applicants herein elect with traverse Group D (claims 46 and 48).

PCT Rule 13.2 states: Where a group of inventions is claimed in one and the same international application, the requirement of unity of invention referred to in Rule 13.1 shall be fulfilled only when there is a technical relationship among those inventions involving one or more of the same or corresponding special technical features.

The elected claims 46 and 48 are directed to the process of producing triacylglycerol. Catalysts occurs with the transfer of fatty acids from phospholipids to diacylglycerol in the production of triacylglycerol through an acyl-CoA independent reaction. Also, the PDAT enzyme of the present invention which is used in the process is characterized through an amino acid conserved consensus sequence as disclosed in the attached table. Therefore, applicants believe all of the claimed sequences should be examined together. Applicants also remind the examiner that the Commissioner has decided *sua sponte* to partially waive the requirements of 37 CFR 1.141 *et seq.* and permit a reasonable number of such nucleotide sequences to be claimed in a single application. MPEP 803.04.

Applicants herein request a two month extension of time.

Please charge any shortage in fees due in connection with the filing of this paper, including Extension of Time fees to Deposit Account No. 11-0345. Please credit any excess fees to such deposit account.

Respectfully submitted,

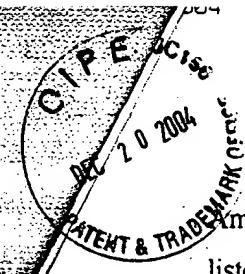
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Amino acids separated by a slash are interchangeably found at this position. Amino acids listed in brackets are found in the large majority of sequences. The relative positions are shown, but one skilled in the art has to expect that variations of 5 to 10 amino acids, in some cases 20 to 30 amino acids in the relative positions of these key residues will occur in some members of the PDAT enzyme family. As an example, residues 115 to 159 of SEQ ID NO.2 were found to be deleted in plant sequences (SEQ ID NO:2a, 3a, 6, 7b, 8, 14 & 15)

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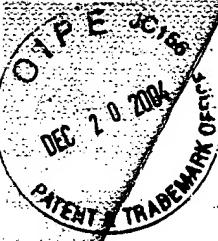


Table X: Amino acid residues connected to PDAT

| Amino acid residue | Position in SEQ ID NO 2 | relative positions |
|--------------------|-------------------------|--------------------|
| V | 25 | 0 |
| E/D | 30 | 5 |
| (H) | 43 | 13 |
| (K) | 44 | 1 |
| (R/K) | 45 | 1 |
| R/K | 64 | 19 |
| K/R | 65 | 1 |
| L/V | 108 | 43 |
| (G) | 160 | 52 |
| (K) | 172 | 12 |
| V/I | 176 | 4 |
| (P) | 179 | 3 |
| (G) | 180 | 1 |
| (P) | 238 | 58 |
| Y | 259 | 21 |
| M/I | 279 | 20 |
| (A) | 282 | 3 |
| Y | 284 | 2 |
| R | 287 | 3 |
| (S/T) | 301 | 14 |
| H | 323 | 22 |
| M/L | 325 | 2 |
| G | 326 | 1 |
| F | 333 | 7 |
| W | 351 | 18 |
| I | 356 | 5 |
| G/A | 364 | 8 |
| G | 368 | 4 |
| S | 378 | 10 |
| G/A | 379 | 1 |
| (P) | 419 | 40 |
| (S/T) | 432 | 13 |
| L/I/V | 498 | 66 |
| (L) | 516 | 18 |
| (P) | 517 | 1 |
| (V) | 530 | 13 |
| (P) | 533 | 3 |
| Y/F | 540 | 7 |
| (V/L) | 573 | 33 |
| P | 604 | 31 |
| G | 611 | 7 |
| G | 612 | 1 |
| (L/M) | 622 | 10 |
| (S/A) | 636 | 14 |